Exhibit A

In the Specification:

-- One class of BT-R_1 allelic variants will be proteins that share a high degree of homology with at least a small region of the amino acid sequence provided in Seq. ID No:[2]2, but may further contain a radical departure from the sequence, such as a non-conservative substitution, truncation, insertion or frame shift. Such alleles are termed mutant alleles of BT-R_1 and represent proteins that typically do not perform the same biological functions as does the BT-R_1 variant of Seq. ID No:2. --

In the Claims:

1. (Amended) A method to identify agents that bind to a BT-toxin receptor, said method comprising the steps of:

(i) contacting an agent with a BT-toxin binding receptor selected from the group consisting of

(a) a cell that has been altered to contain a nucleic acid molecule that encodes a BT toxin receptor having the amino acid sequence of SEQ ID NO:2 and expresses said receptor;[,]

[(b) a cell that has been altered to contain a nucleic acid molecule that encodes a fragment of the amino acid sequence of SEQ ID NO:2 that binds to a BT toxin,]

(b[c]) a cell that has been altered to contain a nucleic acid molecule encoding a BT-toxin receptor that hybridizes to the polynucleotide [nucleic acid] sequence of SEQ ID NO:1 under [high stringency] stringent conditions, wherein said cell expresses said receptor and wherein said receptor has the same sequence as an insect BT toxin receptor that occurs in nature;[,]

[(d) a cell that has been altered to contain a fragment of the nucleic acid molecule that encodes a fragment of a BT-toxin receptor that hybridizes to the nucleic acid sequence of SEQ ID NO:1 under high stringency and that binds to a BT toxin,]